Please replace the paragraph at page 4 lines 15 – 24 with the following paragraph:

-- Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) on the world wide web at ddbj.nig.ac.jp; Genebank on the world wide web at ncbi.nlm.nih.gov/web/Genbank/Index.htlm; and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) on the world wide web at ebi.ac.uk/ebi_docs/embl_db.html. A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12:*76-80 (1994); Birren, *et al., Genome Analysis, 1:*543-559 (1997)).--

Please replace the paragraph at page 29 lines 13 – 24 with the following paragraph:

-- Genomic sequences can be screened for the presence of protein homologues or genes utilizing one or a number of different search algorithms have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and under the section titled "Uses of the Agents of the Invention." In addition, unidentified reading frames may be screened for protein coding regions by prediction software such as GenScan, which is located on the world wide web at gnomic.standford.edu/GENSCANW.html. —

Please replace the paragraph at page 59, line 26, to page 60, line 7, with the following paragraph:

-- Exogenous genetic material may be transferred into a plant cell by the use of a DNA vector or construct designed for such a purpose. Vectors have been engineered for transformation of